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SEQUENCE LISTING

<110> UNIVERSITY COLLEGE LONDON

<120> SCREEN METHOD

<130> N757518

<140> PCT/GB00/00226

<141> 2000-01-26

<150> GB 9901705.5

<151> 1999-01-26

<150> GB 9913066.8

<151> 1999-06-04

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<170> PatentIn Ver. 2.1

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Val Val Arg Ala Leu Pro Glu Ser Leu Cys Gln His Ala Leu Arg Ser
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ctc tac gtg ggc gtg ctg ggc agc aag ctg ggg ctg cag gtg gtg gag 192
Leu Tyr Val Gly Val Leu Gly Ser Lys Leu Gly Leu Gln Val Val Glu
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ctg ccg gcc gac gag agc ctt ccg gac tgc gtc ttc gtg gag gac gtg 240
Leu Pro Ala Asp Glu Ser Leu Pro Asp Cys Val Phe Val Glu Asp Val
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gcc gtg gtg tgc gag gag acg gcc ctc atc acc cga ccc ggg gcg ccg 288
Ala Val Val Cys Glu Glu Thr Ala Leu Ile Thr Arg Pro Gly Ala Pro
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agc cgg agg aag gag gtt gac atg atg aaa gaa gca tta gaa aaa ctt 336
 Ser Arg Arg Lys Glu Val Asp Met Met Lys Glu Ala Leu Glu Lys Leu
 100 105 110

cag ctc aat ata gta gag atg aaa gat gaa aat gca act tta gat ggc 384
 Gln Leu Asn Ile Val Glu Met Lys Asp Glu Asn Ala Thr Leu Asp Gly
 115 120 125

gga gat gtt tta ttc aca ggc aga gaa ttt ttt gtg ggc ctt tcc aaa 432
 Gly Asp Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys
 130 135 140

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 Arg Thr Asn Gln Arg Gly Ala Glu Ile Leu Ala Asp Thr Phe Lys Asp
 145 150 155 160

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 Tyr Ala Val Ser Thr Val Pro Val Ala Asp Gly Leu His Leu Lys Ser
 165 170 175

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 Phe Cys Ser Met Ala Gly Pro Asn Leu Ile Ala Ile Gly Ser Ser Glu
 180 185 190

tct gca cag aag gcc ctt aag atc atg caa cag atg agt gac cac cgc 624
 Ser Ala Gln Lys Ala Leu Lys Ile Met Gln Gln Met Ser Asp His Arg
 195 200 205

tac gac aaa ctc act gtg cct gat gac ata gca gca aac tgt ata tat 672
 Tyr Asp Lys Leu Thr Val Pro Asp Asp Ile Ala Ala Asn Cys Ile Tyr
 210 215 220

cta aat atc ccc aac aaa ggg cac gtc ttg ctg cac cga acc ccg gaa 720
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 225 230 235 240

gag tat cca gaa agt gca aag gtt tat gag aaa ctg aag gac cat atg 768
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ctg atc ccc gtg agc atg tct gaa ctg gaa aag gtg gat ggg ctg ctc 816
 Leu Ile Pro Val Ser Met Ser Glu Leu Glu Lys Val Asp Gly Leu Leu
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acc tgc tgc tca gtt tta att aac aag aag gta gac tcc tga 858
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35 40 45

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50 55 60

Leu Pro Ala Asp Glu Ser Leu Pro Asp Cys Val Phe Val Glu Asp Val
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Ala Val-Val Cys Glu Glu Thr Ala Leu Ile Thr Arg Pro Gly Ala Pro
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Ser Arg Arg Lys Glu Val Asp Met Met Lys Glu Ala Leu Glu Lys Leu
100 105 110

Gln Leu Asn Ile Val Glu Met Lys Asp Glu Asn Ala Thr Leu Asp Gly
115 120 125

Gly Asp Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys
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145 150 155 160

Tyr Ala Val Ser Thr Val Pro Val Ala Asp Gly Leu His Leu Lys Ser
165 170 175

Phe Cys Ser Met Ala Gly Pro Asn Leu Ile Ala Ile Gly Ser Ser Glu
180 185 190

Ser Ala Gln Lys Ala Leu Lys Ile Met Gln Gln Met Ser Asp His Arg
195 200 205

Tyr Asp Lys Leu Thr Val Pro Asp Asp Ile Ala Ala Asn Cys Ile Tyr
210 215 220

Leu Asn Ile Pro Asn Lys Gly His Val Leu Leu His Arg Thr Pro Glu
225 230 235 240

Glu Tyr Pro Glu Ser Ala Lys Val Tyr Glu Lys Leu Lys Asp His Met
245 250 255

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 Arg Gly Val Pro Glu Ser Leu Ala Ser Gly Glu Gly Ala Gly Ala Gly
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 Leu Pro Ala Leu Asp Leu Ala Lys Ala Gln Arg Glu His Gly Val Leu
 35 40 45
 gga ggt aaa ctg agg caa cga ctg ggg cta cag ctg cta gaa ctg cca 192
 Gly Gly Lys Leu Arg Gln Arg Leu Gly Leu Gln Leu Leu Glu Leu Pro
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 Ile Gln Gly Asp Thr Ala Leu Ile Thr Arg Pro Trp Ser Pro Ala Arg
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 Arg Pro Glu Val Asp Gly Val Arg Lys Ala Leu Gln Asp Leu Gly Leu
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 Arg Ile Val Glu Ile Gly Asp Glu Asn Ala Thr Leu Asp Gly Thr Asp
 115 120 125
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 130 135 140
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 Asn His Arg Gly Ala Glu Ile Val Ala Asp Thr Phe Arg Asp Phe Ala
 145 150 155 160
 gtc tcc act gtg cca gtc tcg ggt ccc tcc cac ctg cgc ggt ctc tgc 528
 Val Ser Thr Val Pro Val Ser Gly Pro Ser His Leu Arg Gly Leu Cys
 165 170 175
 ggc atg ggg gga cct cgc act gtt gtg gca ggc agc agc gac gct gcc 576

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caa aag gct gtc cgg gca atg gca gtg ctg aca gat cac cca tat gcc	624
Gln Lys Ala Val Arg Ala Met Ala Val Leu Thr Asp His Pro Tyr Ala	
195 200 205	
tcc ctg acc ctc cca gat gac gca gct gct gac tgt ctc ttt ctt cgt	672
Ser Leu Thr Leu Pro Asp Asp Ala Ala Ala Asp Cys Leu Phe Leu Arg	
210 215 220	
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Pro Gly Leu Pro Gly Val Pro Pro Phe Leu Leu His Arg Gly Gly Gly	
225 230 235 240	
gat ctg ccc aac agc cag gag gca ctg cag aag ctc tct gat gtc acc	768
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245 250 255	
ctg gta cct gtg tcc tgc tca gaa ctg gag aaa gct ggc gcc ggg ctc	816
Leu Val Pro Val Ser Cys Ser Glu Leu Glu Lys Ala Gly Ala Gly Leu	
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Leu Pro Ala Leu Asp Leu Ala Lys Ala Gln Arg Glu His Gly Val Leu
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 50 55 60

Pro Glu Glu Ser Leu Pro Leu Gly Pro Leu Leu Gly Asp Thr Ala Val
 65 70 75 80

Ile Gln Gly Asp Thr Ala Leu Ile Thr Arg Pro Trp Ser Pro Ala Arg
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Arg Pro Glu Val Asp Gly Val Arg Lys Ala Leu Gln Asp Leu Gly Leu
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 115 120 125

Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys Trp Thr
 130 135 140

Asn His Arg Gly Ala Glu Ile Val Ala Asp Thr Phe Arg Asp Phe Ala
 145 150 155 160

Val Ser Thr Val Pro Val Ser Gly Pro Ser His Leu Arg Gly Leu Cys
 165 170 175

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 180 185 190

Gln Lys Ala Val Arg Ala Met Ala Val Leu Thr Asp His Pro Tyr Ala
 195 200 205

Ser Leu Thr Leu Pro Asp Asp Ala Ala Ala Asp Cys Leu Phe Leu Arg
 210 215 220

Pro Gly Leu Pro Gly Val Pro Pro Phe Leu Leu His Arg Gly Gly Gly
 225 230 235 240

Asp Leu Pro Asn Ser Gln Glu Ala Leu Gln Lys Leu Ser Asp Val Thr
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 Glu Gly Leu Val Thr His Val Glu Arg Glu Gln Val Asp His Gly Leu
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Trp Glu Thr Leu Glu Val Asp Pro Ala Glu Tyr Cys Pro Asp Ser Val			
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Phe Val Glu Asp Ala Val Val Phe Arg Asn Val Ala Leu Ile Thr			
65	70	75	80
cgg ccc gcc gcc gag tcg cgg cgc gcc gag acg gcc gcc gtc gag gag			288
Arg Pro Gly Ala Glu Ser Arg Arg Ala Glu Thr Ala Gly Val Glu Glu			
85	90	95	
gcc gtg gcc cgg ctc gcc tgc tcg gtg aac tgg gtg tgg gag ccg gcc			336
Ala Val Ala Arg Leu Gly Cys Ser Val Asn Trp Val Trp Glu Pro Gly			
100	105	110	
acc ctg gac gcc gcc gac gtc ctg aag atc gcc gac acg atc tac gtg			384
Thr Leu Asp Gly Gly Asp Val Leu Lys Ile Gly Asp Thr Ile Tyr Val			
115	120	125	
gga cgc gcc gcc cgg acc aac gcg gcc ggt gtc cag cag ttg cgg gcg			432
Gly Arg Gly Gly Arg Thr Asn Ala Ala Gly Val Gln Gln Leu Arg Ala			
130	135	140	
gcg ttc gag ccg ctg gcc gcc cgg gtc gtc gcc gtg ccc gtg agc aag			480
Ala Phe Glu Pro Leu Gly Ala Arg Val Val Ala Val Pro Val Ser Lys			
145	150	155	160
gtg ctg cat ctg aag tcg gcg gtc acc gcg ctg ccg gac ggg acg gtg			528
Val Leu His Leu Lys Ser Ala Val Thr Ala Leu Pro Asp Gly Thr Val			
165	170	175	
atc ggg cac atc ccg ctg acg gac gtg ccc tcg ctg ttc ccc cgt ttc			576
Ile Gly His Ile Pro Leu Thr Asp Val Pro Ser Leu Phe Pro Arg Phe			
180	185	190	
ctg ccg gtg ccg gag gag tcg ggg gcg cac gtg gtg ctg ctc gcc ggg			624
Leu Pro Val Pro Glu Glu Ser Gly Ala His Val Val Leu Leu Gly Gly			
195	200	205	
agc agg ctg ctg atg gcg gcg agc gcg ccc aag acg gcg gag ctg ctc			672
Ser Arg Leu Leu Met Ala Ala Ser Ala Pro Lys Thr Ala Glu Leu Leu			
210	215	220	
gcc gat ctc ggt cac gag ccg gtg ctc gtc gac atc ggg gag ttc gag			720
Ala Asp Leu Gly His Glu Pro Val Leu Val Asp Ile Gly Glu Phe Glu			
225	230	235	240
aag ctg gag gcc tgt gtg acg tgc ctc tcg gtc agg ctg cgc gag ctg			768
Lys Leu Glu Gly Cys Val Thr Cys Leu Ser Val Arg Leu Arg Glu Leu			
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tac gac tga			777

Tyr Asp

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Ala Leu Glu Gln Trp Asp Ala Tyr Val Glu Ala Leu Gly Ala His Gly
 35 40 45

Trp Glu Thr Leu Glu Val Asp Pro Ala Glu Tyr Cys Pro Asp Ser Val
 50 55 60

Phe Val Glu Asp Ala Val Val Val Phe Arg Asn Val Ala Leu Ile Thr
 65 70 75 80

Arg Pro Gly Ala Glu Ser Arg Arg Ala Glu Thr Ala Gly Val Glu Glu
 85 90 95

Ala Val Ala Arg Leu Gly Cys Ser Val Asn Trp Val Trp Glu Pro Gly
 100 105 110

Thr Leu Asp Gly Gly Asp Val Leu Lys Ile Gly Asp Thr Ile Tyr Val
 115 120 125

Gly Arg Gly Gly Arg Thr Asn Ala Ala Gly Val Gln Gln Leu Arg Ala
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Ala Phe Glu Pro Leu Gly Ala Arg Val Val Ala Val Pro Val Ser Lys
 145 150 155 160

Val Leu His Leu Lys Ser Ala Val Thr Ala Leu Pro Asp Gly Thr Val
 165 170 175

Ile Gly His Ile Pro Leu Thr Asp Val Pro Ser Leu Phe Pro Arg Phe
 180 185 190

Leu Pro Val Pro Glu Glu Ser Gly Ala His Val Val Leu Leu Gly Gly
 195 200 205

Ser Arg Leu Leu Met Ala Ala Ser Ala Pro Lys Thr Ala Glu Leu Leu
 210 215 220

Ala Asp Leu Gly His Glu Pro Val Leu Val Asp Ile Gly Glu Phe Glu
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Gly Leu Thr Ser Ser His Leu Gly Lys Pro Asp Tyr Ala Lys Ala Leu
  20        25        30

gag cag cac aac gcc tac atc cgc gcc ttg cag acc tgc gac gtg gac 144
Glu Gln His Asn Ala Tyr Ile Arg Ala Leu Gln Thr Cys Asp Val Asp
  35        40        45

atc acc ctg ctg ccg ccg gac gaa cgc ttc ccc gac tcg gtg ttc gtc 192
Ile Thr Leu Leu Pro Pro Asp Glu Arg Phe Pro Asp Ser Val Phe Val
  50        55        60

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Glu Asp Pro Val Leu Cys Thr Ser Arg Cys Ala Ile Ile Thr Arg Pro
  65        70        75        80

ggc gcc gaa tcg cgg cgc ggc gag acc gag atc atc gag gaa acc gtg 288
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Gln Arg Phe Tyr Pro Gly Lys Val Glu Arg Ile Glu Ala Pro Gly Thr
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gtg gaa gcc ggc gac atc atg atg gtc ggc gac cac ttc tac atc ggc 384
Val Glu Ala Gly Asp Ile Met Met Val Gly Asp His Phe Tyr Ile Gly
 115       120       125

gaa tcg gcc cgc acc aac gcc gag ggc gcc cgg cag atg atc gcg atc 432
Glu Ser Ala Arg Thr Asn Ala Glu Gly Ala Arg Gln Met Ile Ala Ile
 130       135       140

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Leu Glu Lys His Gly Leu Ser Gly Ser Val Val Arg Leu Glu Lys Val
 145       150       155       160

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180 185 190

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Ile Glu Ile Pro Glu Glu Ser Tyr Ala Ala Asn Cys Ile Trp Val
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Ile Ala Arg Leu Gly Tyr Arg Val Ile Glu Val Asp Thr Ser Glu Tyr
225 230 235 240

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50 55 60

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85 90 95

Gln Arg Phe Tyr Pro Gly Lys Val Glu Arg Ile Glu Ala Pro Gly Thr
100 105 110

Val Glu Ala Gly Asp Ile Met Met Val Gly Asp His Phe Tyr Ile Gly
115 120 125

Glu Ser Ala Arg Thr Asn Ala Glu Gly Ala Arg Gln Met Ile Ala Ile
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 Leu His Leu Lys Thr Gly Leu Ala Tyr Leu Glu His Asn Asn Leu Leu
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 Ala Ala Gly Glu Phe Val Ser Lys Pro Glu Phe Gln Asp Phe Asn Ile
 180 185 190
 Ile Glu Ile Pro Glu Glu Glu Ser Tyr Ala Ala Asn Cys Ile Trp Val
 195 200 205
 Asn Glu Arg Val Ile Met Pro Ala Gly Tyr Pro Arg Thr Arg Glu Lys
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 Asn Gln Ala Lys Arg Asp His Phe Asp Phe Val Thr Lys Met Arg Glu
 50 55 60
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 Arg Gly Ile Asp Val Leu Glu Met His Asn Leu Leu Thr Glu Thr Ile
 65 70 75 80

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115 120 125	
gct gac gac ctg ccc gcc agc gaa ggc gcc aac atc ctc aag atg tac Ala Asp Asp Leu Pro Ala Ser Glu Gly Ala Asn Ile Leu Lys Met Tyr	432
130 135 140	
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145 150 155 160	
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260 265 270	
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275 280 285	
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 370 375 380

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 385 390 395 400

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 1 5 10 15

Leu Arg Lys Val Met Val Cys Ser Pro Gly Leu Ala His Gln Arg Leu
 20 25 30

Thr Pro Ser Asn Cys Asp Glu Leu Leu Phe Asp Asp Val Ile Trp Val
 35 40 45

Asn Gln Ala Lys Arg Asp His Phe Asp Phe Val Thr Lys Met Arg Glu
 50 55 60

Arg Gly Ile Asp Val Leu Glu Met His Asn Leu Leu Thr Glu Thr Ile
 65 70 75 80

Gln Asn Pro Glu Ala Leu Lys Trp Ile Leu Asp Arg Lys Ile Thr Ala
 85 90 95

Asp Ser Val Gly Leu Gly Leu Thr Ser Glu Leu Arg Ser Trp Leu Glu
 100 105 110
 Ser Leu Glu Pro Arg Lys Leu Ala Glu Tyr Leu Ile Gly Gly Val Ala
 115 120 125
 Ala Asp Asp Leu Pro Ala Ser Glu Gly Ala Asn Ile Leu Lys Met Tyr
 130 135 140
 Arg Glu Tyr Leu Gly His Ser Ser Phe Leu Leu Pro Pro Leu Pro Asn
 145 150 155 160
 Thr Gln Phe Thr Arg Asp Thr Thr Cys Trp Ile Tyr Gly Gly Val Thr
 165 170 175
 Leu Asn Pro Met Tyr Trp Pro Ala Arg Arg Gln Glu Thr Leu Leu Thr
 180 185 190
 Thr Ala Ile Tyr Lys Phe His Pro Glu Phe Ala Asn Ala Glu Phe Glu
 195 200 205
 Ile Trp Tyr Gly Asp Pro Asp Lys Asp His Gly Ser Ser Thr Leu Glu
 210 215 220
 Gly Gly Asp Val Met Pro Ile Gly Asn Gly Val Val Leu Ile Gly Met
 225 230 235 240
 Gly Glu Arg Ser Ser Arg Gln Ala Ile Gly Gln Val Ala Gln Ser Leu
 245 250 255
 Phe Ala Lys Gly Ala Ala Glu Arg Val Ile Val Ala Gly Leu Pro Lys
 260 265 270
 Ser Arg Ala Ala Met His Leu Asp Thr Val Phe Ser Phe Cys Asp Arg
 275 280 285
 Asp Leu Val Thr Val Phe Pro Glu Val Val Lys Glu Ile Val Pro Phe
 290 295 300
 Ser Leu Arg Pro Asp Pro Ser Ser Pro Tyr Gly Met Asn Ile Arg Arg
 305 310 315 320
 Glu Glu Lys Thr Phe Leu Glu Val Val Ala Glu Ser Leu Gly Leu Lys
 325 330 335
 Lys Leu Arg Val Val Glu Thr Gly Gly Asn Ser Phe Ala Ala Glu Arg
 340 345 350
 Glu Gln Trp Asp Asp Gly Asn Asn Val Val Cys Leu Glu Pro Gly Val
 355 360 365
 Val Val Gly Tyr Asp Arg Asn Thr Tyr Thr Asn Thr Leu Leu Arg Lys
 370 375 380
 Ala Gly Val Glu Val Ile Thr Ile Ser Ala Ser Glu Leu Gly Arg Gly

385 390 395 400
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 405 410 415

Asp Tyr

<210> 11
 <211> 1014
 <212> DNA
 <213> M. tuberculosis

<220>
 <221> CDS
 <222> (69)..(986)

<400> 11
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 gttggttt atg acg gat tcc tac gtc gct gct gcc cgt cta ggg tca cct 110
 Met Thr Asp Ser Tyr Val Ala Ala Ala Arg Leu Gly Ser Pro
 1 5 10
 gca cgc cgc acc ccc cgg acg cgg cgg tat gca atg acc ccg ccg gcc 158
 Ala Arg Arg Thr Pro Arg Thr Arg Arg Tyr Ala Met Thr Pro Pro Ala
 15 20 25 30
 ttc ttt gcc gtc gca tac gcg atc aac ccc tgg atg gac gtc acc gcg 206
 Phe Phe Ala Val Ala Tyr Ala Ile Asn Pro Trp Met Asp Val Thr Ala
 35 40 45
 cca gtc gac gtc caa gtc gcg caa gca cag tgg gag cac ctc cac cag 254
 Pro Val Asp Val Gln Val Ala Gln Ala Gln Trp Glu His Leu His Gln
 50 55 60
 acc tat ctt cgg cta ggc cac agc gtg gat ctg atc gag ccc att tcc 302
 Thr Tyr Leu Arg Leu Gly His Ser Val Asp Leu Ile Glu Pro Ile Ser
 65 70 75
 ggg tta ccg gac atg gtg tac acc gcc aac ggt ggg ttc atc gcg cac 350
 Gly Leu Pro Asp Met Val Tyr Thr Ala Asn Gly Gly Phe Ile Ala His
 80 85 90
 gac atc gcc gtg gtc gcc cgg ttc cgg ttc ccc gaa cga gct ggt gag 398
 Asp Ile Ala Val Val Ala Arg Phe Arg Phe Pro Glu Arg Ala Gly Glu
 95 100 105 110
 tct aga gcc tat gcc agc tgg atg tcc tcg gtc gga tat cgc ccg gtg 446
 Ser Arg Ala Tyr Ala Ser Trp Met Ser Ser Val Gly Tyr Arg Pro Val
 115 120 125
 acc acc cgc cac gtc aac gag gga cag gcc gac ctg ctg atg gtt gcc 494
 Thr Thr Arg His Val Asn Glu Gly Gln Gly Asp Leu Leu Met Val Gly

130	135	140	
gaa agg gtg ttg gcg ggc tac ggc ttt cgc aca gac cag cgc gca cac	542		
Glu Arg Val Leu Ala Gly Tyr Gly Phe Arg Thr Asp Gln Arg Ala His			
145	150	155	
gcc gaa atc gcc gcg gtg ctt ggt ctg ccg gtg gtc tcc ctc gag ttg	590		
Ala Glu Ile Ala Ala Val Leu Gly Leu Pro Val Val Ser Leu Glu Leu			
160	165	170	
gtc gac cca cgg ttc tat cac ctg gac acc gcg ctg gcc gtg ctc gac	638		
Val Asp Pro Arg Phe Tyr His Leu Asp Thr Ala Leu Ala Val Leu Asp			
175	180	185	190
gac cac acg atc gcc tac tac ccg ccg gcg ttc agt acg gca gcg cag	686		
Asp His Thr Ile Ala Tyr Tyr Pro Pro Ala Phe Ser Thr Ala Ala Gln			
195	200	205	
gaa cag ttg tcg gcg ctg ttc ccc gac gcg att gtg gtc ggc agt gcc	734		
Glu Gln Leu Ser Ala Leu Phe Pro Asp Ala Ile Val Val Gly Ser Ala			
210	215	220	
gac gcg ttc gtg ttc gga ctc aac gcc gtc tct gac ggt ctg aac gta	782		
Asp Ala Phe Val Phe Gly Leu Asn Ala Val Ser Asp Gly Leu Asn Val			
225	230	235	
gtg ctt ccg gtc gcg gcc atg ggt ttt gcg gcg cag tta cgc gca gcc	830		
Val Leu Pro Val Ala Ala Met Gly Phe Ala Ala Gln Leu Arg Ala Ala			
240	245	250	
ggc ttc gag ccg gtc ggt gtc gat ctg tcc gag ctg ctc aag ggc ggc	878		
Gly Phe Glu Pro Val Gly Val Asp Leu Ser Glu Leu Leu Lys Gly Gly			
255	260	265	270
ggt tcc gtc aag tgc tgc acg ctg gag ata cac cca tga caa atc tcg	926		
Gly Ser Val Lys Cys Cys Thr Leu Glu Ile His Pro Gln Ile Ser			
275	280	285	
cgg atg cca ctc agg cca cta tgg cac tgg tcg aaa ggc atg cag cgc	974		
Arg Met Pro Leu Arg Pro Leu Trp His Trp Ser Lys Gly Met Gln Arg			
290	295	300	
aca att att cgc cgctgcctgt ggtggcggcc agcgctga	1014		
Thr Ile Ile Arg			
305			

<210> 12

<211> 282

<212> PRT

<213> M. tuberculosis

<400> 12

Met	Thr	Asp	Ser	Tyr	Val	Ala	Ala	Ala	Arg	Leu	Gly	Ser	Pro	Ala	Arg
1					5					10				15	

Arg Thr Pro Arg Thr Arg Arg Tyr Ala Met Thr Pro Pro Ala Phe Phe
 20 25 30

Ala Val Ala Tyr Ala Ile Asn Pro Trp Met Asp Val Thr Ala Pro Val
 35 40 45

Asp Val Gln Val Ala Gln Ala Gln Trp Glu His Leu His Gln Thr Tyr
 50 55 60

Leu Arg Leu Gly His Ser Val Asp Leu Ile Glu Pro Ile Ser Gly Leu
 65 70 75 80

Pro Asp Met Val Tyr Thr Ala Asn Gly Gly Phe Ile Ala His Asp Ile
 85 90 95

Ala Val Val Ala Arg Phe Arg Phe Pro Glu Arg Ala Gly Glu Ser Arg
 100 105 110

Ala Tyr Ala Ser Trp Met Ser Ser Val Gly Tyr Arg Pro Val Thr Thr
 115 120 125

Arg His Val Asn Glu Gly Gln Gly Asp Leu Leu Met Val Gly Glu Arg
 130 135 140

Val Leu Ala Gly Tyr Gly Phe Arg Thr Asp Gln Arg Ala His Ala Glu
 145 150 155 160

Ile Ala Ala Val Leu Gly Leu Pro Val Val Ser Leu Glu Leu Val Asp
 165 170 175

Pro Arg Phe Tyr His Leu Asp Thr Ala Leu Ala Val Leu Asp Asp His
 180 185 190

Thr Ile Ala Tyr Tyr Pro Pro Ala Phe Ser Thr Ala Ala Gln Glu Gln
 195 200 205

Leu Ser Ala Leu Phe Pro Asp Ala Ile Val Val Gly Ser Ala Asp Ala
 210 215 220

Phe Val Phe Gly Leu Asn Ala Val Ser Asp Gly Leu Asn Val Val Leu
 225 230 235 240

Pro Val Ala Ala Met Gly Phe Ala Ala Gln Leu Arg Ala Ala Gly Phe
 245 250 255

Glu Pro Val Gly Val Asp Leu Ser Glu Leu Leu Lys Gly Gly Gly Ser
 260 265 270

Val Lys Cys Cys Thr Leu Glu Ile His Pro
 275 280

<210> 13
 <211> 305
 <212> PRT

<213> M. tuberculosis

<400> 13

Asn Val Ser Met Glu Asn Thr Gln Arg Pro Ser Phe Asp Cys Glu Ile
1 5 10 15

Arg Ala Lys Tyr Arg Trp Phe Met Thr Asp Ser Tyr Val Ala Ala Ala
20 25 30

Arg Leu Gly Ser Pro Ala Arg Arg Thr Pro Arg Thr Arg Arg Tyr Ala
35 40 45

Met Thr Pro Pro Ala Phe Phe Ala Val Ala Tyr Ala Ile Asn Pro Trp
50 55 60

Met Asp-Val Thr Ala Pro Val Asp Val Gln Val Ala Gln Ala Gln Trp
65 70 75 80

Glu His Leu His Gln Thr Tyr Leu Arg Leu Gly His Ser Val Asp Leu
85 90 95

Ile Glu Pro Ile Ser Gly Leu Pro Asp Met Val Tyr Thr Ala Asn Gly
100 105 110

Gly Phe Ile Ala His Asp Ile Ala Val Val Ala Arg Phe Arg Phe Pro
115 120 125

Glu Arg Ala Gly Glu Ser Arg Ala Tyr Ala Ser Trp Met Ser Ser Val
130 135 140

Gly Tyr Arg Pro Val Thr Thr Arg His Val Asn Glu Gly Gln Gly Asp
145 150 155 160

Leu Leu Met Val Gly Glu Arg Val Leu Ala Gly Tyr Gly Phe Arg Thr
165 170 175

Asp Gln Arg Ala His Ala Glu Ile Ala Ala Val Leu Gly Leu Pro Val
180 185 190

Val Ser Leu Glu Leu Val Asp Pro Arg Phe Tyr His Leu Asp Thr Ala
195 200 205

Leu Ala Val Leu Asp Asp His Thr Ile Ala Tyr Tyr Pro Pro Ala Phe
210 215 220

Ser Thr Ala Ala Gln Glu Gln Leu Ser Ala Leu Phe Pro Asp Ala Ile
225 230 235 240

Val Val Gly Ser Ala Asp Ala Phe Val Phe Gly Leu Asn Ala Val Ser
245 250 255

Asp Gly Leu Asn Val Val Leu Pro Val Ala Ala Met Gly Phe Ala Ala
260 265 270

Gln Leu Arg Ala Ala Gly Phe Glu Pro Val Gly Val Asp Leu Ser Glu

275		280		285											
Leu	Leu	Lys	Gly	Gly	Gly	Ser	Val	Lys	Cys	Cys	Thr	Leu	Glu	Ile	His
290						295						300			

Pro
305

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: UNIVERSITY COLLEGE LONDON
(B) STREET: Gower Street
(C) CITY: London
(E) COUNTRY: United Kingdom
(F) POSTAL CODE (ZIP): WC1E 6BT

(ii) TITLE OF INVENTION: SCREEN METHOD

(iii) NUMBER OF SEQUENCES: 12

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 858 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATGGCCGGCC TGGCCACCC CTCGCTTC GCGCGGCCA CCCACCCGT GGTGCGGCG	60
CTACCCGAGT CGCTCTGCA GCACGCGTG AGAAGCGCA AGGCGAGGA GGTGACGTC	120
GCCCGCGCGG AACCGCAGCA CCAGCTCTAC GTGGCGGTGC TGGGCAGCA GCTGGGCTG	180
CAGTGGTGG AGTGCCCGC CGACGAGAG CTTCCGACT GCGTCTTCT GGAGGACGTG	240
GCGTGGTGT GCGAGGAGAC GGCCTCATC ACCCGACCG GGGCGCGAG CCGGAGGAAG	300
GAGTTGACA TGATGAAAG AGCATTAGAA AAATTTCAG TCAATATAG AGAGATGAAA	360
GATGAAATG CACTTTAGA TGGCGGAGT GTTTATTCA CAGGCAGAG ATTTTGTG	420
GGCCTTCCA AAAGBACAA TCAACAGGT GCTGAAATCT TGGCTGATC TTTTAAGGAC	480

TATGCAGTCT CCACAGTGCC AGTGSCAGAT GGGTTGCATT TGAAGAGTTT CTGCAGCATG 540
 GCTGGGCCTA ACCTGATCGC AATTGGGTCT AGTGAATCTG CACAGAAGGC CCTTAAGATC 600
 ATGCAACAGA TGAGTGACCA CGCTACGAC AAACCTACTG TGCTGATGA CATAGCAGCA 660
 AACTGTATAT ATCTAAATAT CCCCACAAA GGGCACGTCT TGCTGCACCG AACCCCGGAA 720
 GAGTATCCAG AAAGTGCAA GGTATTATGAG AAACCTGAAG ACCATATGCT GATCCCGGTG 780
 AGCATGTCTG AACTGGAAAA GGTGGATGGG CTGCTCACCT GCTGCTCAGT TTTAATTAAC 840
 AAGAAGGTAG ACTCCTGA 858

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Gly Leu Gly His Pro Ser Ala Phe Gly Arg Ala Thr His Ala
 1 5 10 15
 Val Val Arg Ala Leu Pro Glu Ser Leu Cys Gln His Ala Leu Arg Ser
 20 25 30
 Ala Lys Gly Glu Glu Val Asp Val Ala Arg Ala Glu Arg Gln His Gln
 35 40 45
 Leu Tyr Val Gly Val Leu Gly Ser Lys Leu Gly Leu Gln Val Val Glu
 50 55 60
 Leu Pro Ala Asp Glu Ser Leu Pro Asp Cys Val Phe Val Glu Asp Val
 65 70 75 80
 Ala Val Val Cys Glu Glu Thr Ala Leu Ile Thr Arg Pro Gly Ala Pro
 85 90 95
 Ser Arg Arg Lys Glu Val Asp Met Met Lys Glu Ala Leu Glu Lys Leu
 100 105 110
 Gln Leu Asn Ile Val Glu Met Lys Asp Glu Asn Ala Thr Leu Asp Gly
 115 120 125

Gly Asp Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys
 130 135 140
 Arg Thr Asn Gln Arg Gly Ala Glu Ile Leu Ala Asp Thr Phe Lys Asp
 145 150 155 160
 Tyr Ala Val Ser Thr Val Pro Val Ala Asp Gly Leu His Leu Lys Ser
 165 170 175
 Phe Cys Ser Met Ala Gly Pro Asn Leu Ile Ala Ile Gly Ser Ser Glu
 180 185 190
 Ser Ala Gln Lys Ala Leu Lys Ile Met Gln Gln Met Ser Asp His Arg
 195 200 205
 Tyr Asp Lys Leu Thr Val Pro Asp Asp Ile Ala Ala Asn Cys Ile Tyr
 210 215 220
 Leu Asn Ile Pro Asn Lys Gly His Val Leu Leu His Arg Thr Pro Glu
 225 230 235 240
 Glu Tyr Pro Glu Ser Ala Lys Val Tyr Glu Lys Leu Lys Asp His Met
 245 250 255
 Leu Ile Pro Val Ser Met Ser Glu Leu Glu Lys Val Asp Gly Leu Leu
 260 265 270
 Thr Cys Cys Ser Val Leu Ile Asn Lys Lys Val Asp Ser
 275 280 285

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 858 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATGGGGACGC CGGGGGAGGG GCTGGGCCGC TGCTCCCATG CCCTGATCCG GGGAGTCCCA	60
GAGAGCCTGG CGTCGGGGGA AGGTGCGGGG GCTGGCCTTC CCCTCTGGA TCTGGCCAAA	120
GCTCAAAGGG AGCACGGGT GCTGGGAGGT AAAGTGGGC AACGACTGGG GCTACAGCTG	180
CTAGAACTGC CACCTGAGGA GTCATTGCCG CTGGGACCBC TGCTTGGCGA CACGGCCGTG	240
ATCCAAGGGG ACACGGCCCT AATCACGCGG CCTGSGAGCC CCGCTGTAG GCCAGAGGTC	300

GATGGAGTCC GCAAAGCCCT GCAAGACCTG GGGCTCCGAA TTGTGGAAT AGGAGACGAG	360
AACGCGACGC TGGATGACAC TGACGTTCTC TTCACCGGCC GGGAGTTTTT CGTAGGCCTC	420
TCCAAATGGA CCAATCACCG AGGAGCTGAG ATGCTGGCGG ACACGTTCCG GGACTTCGCC	480
GTCTCCACTG TGCCAGTCTC GGCTCCCTCC CACCTGCGCG GTCTCTGCGG CATGGGGGGA	540
CCTCGCACTG TTGTGGCAGG CAGCAGCAGC GCTGCCCAAA AGGCTGTCCG GGCAATGGCA	600
GTGCTGACAG ATCACCATA TGCCTCCCTG ACCCTCCAG ATGACGCAGC TGCTGACTGT	660
CTCTTCTCTC GTCTGGGTT GCCTGGTGTG CCCCCTTTCC TCCTGCACCG TGGAGGTGGG	720
GATCTGCCCA ACAGCCAGGA GGCACTGCAG AAGCTCTCTG ATGTCACCCT GGTACCTGTG	780
TCCTGCTCAG AACTGGAGAA AGCTGGCGCC GGGCTCAGCT CCCTCTGCTT GGTGCTCAGC	840
ACACGCCCCC ACAGCTGA	858

(2) INFORMATION FOR SEQ ID NO: 4:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Gly	Thr	Pro	Gly	Glu	Gly	Leu	Gly	Arg	Cys	Ser	His	Ala	Leu	Ile
1				5				10						15	
Arg	Gly	Val	Pro	Glu	Ser	Leu	Ala	Ser	Gly	Glu	Gly	Ala	Gly	Ala	Gly
		20					25						30		
Leu	Pro	Ala	Leu	Asp	Leu	Ala	Lys	Ala	Gln	Arg	Glu	His	Gly	Val	Leu
	35					40						45			
Gly	Gly	Lys	Leu	Arg	Gln	Arg	Leu	Gly	Leu	Gln	Leu	Glu	Leu	Pro	
	50				55					60					
Pro	Glu	Glu	Ser	Leu	Pro	Leu	Gly	Pro	Leu	Leu	Gly	Asp	Thr	Ala	Val
65				70				75						80	
Ile	Gln	Gly	Asp	Thr	Ala	Leu	Ile	Thr	Arg	Pro	Trp	Ser	Pro	Ala	Arg
		85					90							95	
Arg	Pro	Glu	Val	Asp	Gly	Val	Arg	Lys	Ala	Leu	Gln	Asp	Leu	Gly	Leu

-5-

100	105	110
Arg Ile Val Glu Ile Gly Asp Glu Asn Ala Thr Leu Asp Gly Thr Asp		
115	120	125
Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys Trp Thr		
130	135	140
Asn His Arg Gly Ala Glu Ile Val Ala Asp Thr Phe Arg Asp Phe Ala		
145	150	155
Val Ser Thr Val Pro Val Ser Gly Pro Ser His Leu Arg Gly Leu Cys		
165	170	175
Gly Met Gly Gly Pro Arg Thr Val Val Ala Gly Ser Ser Asp Ala Ala		
180	185	190
Gln Lys Ala Val Arg Ala Met Ala Val Leu Thr Asp His Pro Tyr Ala		
195	200	205
Ser Leu Thr Leu Pro Asp Asp Ala Ala Ala Asp Cys Leu Phe Leu Arg		
210	215	220
Pro Gly Leu Pro Gly Val Pro Pro Phe Leu Leu His Arg Gly Gly Gly		
225	230	235
Asp Leu Pro Asn Ser Gln Glu Ala Leu Gln Lys Leu Ser Asp Val Thr		
245	250	255
Leu Val Pro Val Ser Cys Ser Glu Leu Glu Lys Ala Gly Ala Gly Leu		
260	265	270
Ser Ser Leu Cys Leu Val Leu Ser Thr Arg Pro His Ser		
275	280	285

(2) INFORMATION FOR SEQ ID NO: 5:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 777 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GTGCCCAGCA AGAAGGCCCT GGTCCGCCGC CCCAGCCCCA GGCTCGCGGA AGGACTGGTG 60


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ACACACGTCG AGCGGGAGCA GGTCSATCAC GGCCTGGCCC TCGAACAGTG GGACGCCTAC   120
GTCGAGGCCC TCGGAGCACA CGGCTGGGAG ACTCTGGAGG TGGACCCGGC CGAGTACTGT   180
CCGGAATCGG TCTTCGTGCA GGACGCCGTC GTCTGTTCCT GCAACGTGCG GCTGATCAGG   240
CGGCCCGGCG CCGAGTCGCG GCGCGCGGAG ACGGCCGGCG TCGAGGAGGC CGTGGCCCGG   300
CTCGGTGCTT CCGTGAAC TGTTGTGGAG CCGGECACCC TGGACGGCGG CGAGTCTCTG   360
AAGATCGGCG ACACGATCTA CGTGGGACGC GGCGGCCGGA CCAACGCGGC CGGTGTCCAG   420
CAGTTGCGGG CCGCGTTCGA GCGCTGGGCG GCCCGGGTCG TCGCCGTGCC CGTGAGCAAG   480
GTGCTGCATC TGAAGTCGGC GGTACCCGCG CTGCGGACG GGACGGTGAT CCGGCACATC   540
CCGCTGACGG ACGTGCCTTC GCTGTTCCCG CGTTTCCTGC CCGTGCCGGA GGAGTCGGGG   600
GCGCACGTGG TGTGCTCGG CCGGAGCAGG CTGCTGATGG CCGCGAGCGC GCCCAAGACG   660
CGGAGCTGTC TCGCGGATCT CCGTCACGAG CCGGTGCTCG TCGACATCGG GGAGTTCGAG   720
AAGCTGGAGG GCTGTGTGAC GTGCCTCTCG GTCAGGCTGC GCGAGCTGTA CGACTGA    777

```

(2) INFORMATION FOR SEQ ID NO: 6:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```

Val Pro Ser Lys Lys Ala Leu Val Arg Arg Pro Ser Pro Arg Leu Ala
1           5           10          15

Glu Gly Leu Val Thr His Val Glu Arg Glu Gln Val Asp His Gly Leu
20          25          30

Ala Leu Glu Gln Trp Asp Ala Tyr Val Glu Ala Leu Gly Ala His Gly
35          40          45

Trp Glu Thr Leu Glu Val Asp Pro Ala Glu Tyr Cys Pro Asp Ser Val
50          55          60

Phe Val Glu Asp Ala Val Val Val Phe Arg Asn Val Ala Leu Ile Thr

```

-7-

65 70 75 80
 Arg Pro Gly Ala Glu Ser Arg Arg Ala Glu Thr Ala Gly Val Glu Glu
 85 90 95
 Ala Val Ala Arg Leu Gly Cys Ser Val Asn Trp Val Trp Glu Pro Gly
 100 105 110
 Thr Leu Asp Gly Gly Asp Val Leu Lys Ile Gly Asp Thr Ile Tyr Val
 115 120 125
 Gly Arg Gly Gly Arg Thr Asn Ala Ala Gly Val Gln Gln Leu Arg Ala
 130 135 140
 Ala Phe Glu Pro Leu Gly Ala Arg Val Val Ala Val Pro Val Ser Lys
 145 150 155 160
 Val Leu His Leu Lys Ser Ala Val Thr Ala Leu Pro Asp Gly Thr Val
 165 170 175
 Ile Gly His Ile Pro Leu Thr Asp Val Pro Ser Leu Phe Pro Arg Phe
 180 185 190
 Leu Pro Val Pro Glu Glu Ser Gly Ala His Val Val Leu Leu Gly Gly
 195 200 205
 Ser Arg Leu Leu Met Ala Ala Ser Ala Pro Lys Thr Ala Glu Leu Leu
 210 215 220
 Ala Asp Leu Gly His Glu Pro Val Leu Val Asp Ile Gly Glu Phe Glu
 225 230 235 240
 Lys Leu Glu Gly Cys Val Thr Cys Leu Ser Val Arg Leu Arg Glu Leu
 245 250 255
 Tyr Asp

(2) INFORMATION FOR SEQ ID NO: 7:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATGTTCAAGC ACATCATCGC TCGCAGCCCC GCCCGCAGCC TGGTCGACGG CCTGACCTCC 60

```

AGCCACCTCG GCAAGCCGGA CTACGCCAAG GCCCTGAGC AGCACAACGC CTACATCCGC 120
GCCTTGCGA CTTGCGAGCT GGACATCACC CTGCTGCCG CGGACGAACG CTTCCCGGAC 180
TCGTTGTTG TCGAGGACCC GGTGCTCTGC ACCTCGCGCT GCGCATCAT CACCCGCCCC 240
GGCGCCGAAT CGCGCGCGG CGAGACCGAG ATCATCGAGG AAACCGTGA GCGTTCTAT 300
CCGGGCAAGG TCGAGCGCAT CGAGGCACC GGCACGCTG AAGCCGGCG CATCATGATG 360
GTGCGGACC ACTTCTACAT CGGCGAATCG GCCCGACCA ACGCCGAGG CGCCGGCAG 420
ATGATCGCGA TCCTGGAGAA ACATGGCCTC AGCGGCTCG TGTGCGCCT GGAAGGTC 480
CTGCACCTGA AGACCGGCT CGCCTACCTG GAACACAACA ACCTGCTGGC CGCGCGGAG 540
TTGTCAGCA AGCCGGAGTT CCAGGACTTC AACATCATCG AGATCCCCGA AGAGGATCC 600
TACGCCGCA ACTGCATCTG GGTCAACGAA AGGTGATCA TGCCCGCGG CTATCCCGG 660
ACCCGCGAGA AGATCGCCG CCTCGGCTAC CGGTGATCG AGGTGGACAC CTCGAATAT 720
CGCAAGATCG ACGCGCGCT CASTTGATG TCGTGGCT TCTGA 765

```

(2) INFORMATION FOR SEQ ID NO: 8:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```

Met Phe Lys His Ile Ile Ala Arg Thr Pro Ala Arg Ser Leu Val Asp
1           5           10          15
Gly Leu Thr Ser Ser His Leu Gly Lys Pro Asp Tyr Ala Lys Ala Leu
20          25          30
Glu Gln His Asn Ala Tyr Ile Arg Ala Leu Gln Thr Cys Asp Val Asp
35          40          45
Ile Thr Leu Leu Pro Pro Asp Glu Arg Phe Pro Asp Ser Val Phe Val
50          55          60
Glu Asp Pro Val Leu Cys Thr Ser Arg Cys Ala Ile Ile Thr Arg Pro
65          70          75          80

```

Gly Ala Glu Ser Arg Arg Gly Glu Thr Glu Ile Ile Glu Glu Thr Val
 85 90 95
 Gln Arg Phe Tyr Pro Gly Lys Val Glu Arg Ile Glu Ala Pro Gly Thr
 100 105 110
 Val Glu Ala Gly Asp Ile Met Met Val Gly Asp His Phe Tyr Ile Gly
 115 120 125
 Glu Ser Ala Arg Thr Asn Ala Glu Gly Ala Arg Gln Met Ile Ala Ile
 130 135 140
 Leu Glu Lys His Gly Leu Ser Gly Ser Val Val Arg Leu Glu Lys Val
 145 150 155 160
 Leu His Leu Lys Thr Gly Leu Ala Tyr Leu Glu His Asn Asn Leu Leu
 165 170 175
 Ala Ala Gly Glu Phe Val Ser Lys Pro Glu Phe Gln Asp Phe Asn Ile
 180 185 190
 Ile Glu Ile Pro Glu Glu Glu Ser Tyr Ala Ala Asn Cys Ile Trp Val
 195 200 205
 Asn Glu Arg Val Ile Met Pro Ala Gly Tyr Pro Arg Thr Arg Glu Lys
 210 215 220
 Ile Ala Arg Leu Gly Tyr Arg Val Ile Glu Val Asp Thr Ser Glu Tyr
 225 230 235 240
 Arg Lys Ile Asp Gly Gly Val Ser Cys Met Ser Leu Arg Phe
 245 250

(2) INFORMATION FOR SEQ ID NO: 9:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATGAGCACGG AAAAAACAA ACTTGGCGTC CACTCCGAAG CCGGCAAACT GCGCAAAGTG	60
ATGGTCTGCT CGCCCGGACT CGCCACCAG CGCCTGACCC CGAGCAACTG CGACGAGTTG	120
CTGTTGACG ACCTGATCTG GGTGAACCAG GCCAAGCGCG ACCACTTCGA CTTCGTGACC	180

AAGATGCGCG AGCGCGCAT CGACGTCTC GAGATGCACA ATCTGCTGAC CGAGACCATC	240
CAGAACCCGG AAGCGCTGAA GTGGATCCTC GATCGCAAGA TCACGCGGA CAGCGTCGGC	300
CTGGGCTGA CCAGCGAGCT GCGTCTCTGG CTGGAGAGCC TGGAGCCGCG CAAGCTGGCC	360
GASTACCTGA TCGGCGGCT CGCCGCTGAC GACCTGCCCG CCAGCGAAGG CGCCAACATC	420
CTCAAGATGT ACCGCGAGTA CCTGGGCCAT TCCAGTTTC TCGTCCGCG GTTGCCGAAC	480
ACCCAGTTCA CCGCGACAC CACTTGCTGG ATCTACGGCG GCGTGACCCT GAACCCGATG	540
TACTGGCCGG CGGACGACA GSAACCTG CTGACCAGCG CCATCTACAA GTTCCACCCC	600
GASTTCGCCA ACGCCGAGT CGAGATCTGG TACGGCGACC CGGACAAGGA CCACGGCTCC	660
TCGACCTGG AAGCGCGGA CGTGATGCCG ATCGGCAACG GCGTGTCTCT GATCGGCATG	720
GGCGAGCGCT CCTCGGCCA GGCCATCGGT CAGGTGCGCC AGTGGCTGTT CGCCAAGGGC	780
GCCGCGAGC GGGTGATCGT CGCCGGCTG CCGAAGTCC GCGCGCGAT GCACCTGGAC	840
ACCGTGTTC GCTTCTGGA CCGCGACCTG GTCAGGTCT TCCCGAAGT GGTCAAGGAA	900
ATCGTGCCCT TCAGCTGCG CCCGATCGG AGCAGCCCTT ACGCATGAA CATCGCCCGC	960
GAGGAGAAAA CCTTCTCGA AGTGGTCGCC GAATCCCTCG GCTGAAGAA ACTGCGCGTG	1020
GTGAGACCG GCGCAACAG CTTGCGCGC GAGCGGAGC AATGGGACGA CGTAACAAC	1080
GTGGTCTGCC TGGAGCGGG CGTGGTGGTC GGCTACGACC GCAACACCTA CACCAACACC	1140
CTGCTGCGCA AGGCCGGCT CGAGGTCATC ACCATCAGCG CCAGCGAACT GGGTCGCGGT	1200
CGCGGGGGG GCCACTGCAT GACCTGCCCG ATCGTCCGCG ACCCGATCGA CTACTGA	1257

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met	Ser	Thr	Glu	Lys	Thr	Lys	Leu	Gly	Val	His	Ser	Glu	Ala	Gly	Lys
1				5				10						15	

Leu Arg Lys Val Met Val Cys Ser Pro Gly Leu Ala His Gln Arg Leu
 20 25 30
 Thr Pro Ser Asn Cys Asp Glu Leu Leu Phe Asp Asp Val Ile Trp Val
 35 40 45
 Asn Gln Ala Lys Arg Asp His Phe Asp Phe Val Thr Lys Met Arg Glu
 50 55 60
 Arg Gly Ile Asp Val Leu Glu Met His Asn Leu Leu Thr Glu Thr Ile
 65 70 75 80
 Gln Asn Pro Glu Ala Leu Lys Trp Ile Leu Asp Arg Lys Ile Thr Ala
 85 90 95
 Asp Ser Val Gly Leu Gly Leu Thr Ser Glu Leu Arg Ser Trp Leu Glu
 100 105 110
 Ser Leu Glu Pro Arg Lys Leu Ala Glu Tyr Leu Ile Gly Gly Val Ala
 115 120 125
 Ala Asp Asp Leu Pro Ala Ser Glu Gly Ala Asn Ile Leu Lys Met Tyr
 130 135 140
 Arg Glu Tyr Leu Gly His Ser Ser Phe Leu Leu Pro Pro Leu Pro Asn
 145 150 155 160
 Thr Gln Phe Thr Arg Asp Thr Thr Cys Trp Ile Tyr Gly Gly Val Thr
 165 170 175
 Leu Asn Pro Met Tyr Trp Pro Ala Arg Arg Gln Glu Thr Leu Leu Thr
 180 185 190
 Thr Ala Ile Tyr Lys Phe His Pro Glu Phe Ala Asn Ala Glu Phe Glu
 195 200 205
 Ile Trp Tyr Gly Asp Pro Asp Lys Asp His Gly Ser Ser Thr Leu Glu
 210 215 220
 Gly Gly Asp Val Met Pro Ile Gly Asn Gly Val Val Leu Ile Gly Met
 225 230 235 240
 Gly Glu Arg Ser Ser Arg Gln Ala Ile Gly Gln Val Ala Gln Ser Leu
 245 250 255
 Phe Ala Lys Gly Ala Ala Glu Arg Val Ile Val Ala Gly Leu Pro Lys
 260 265 270
 Ser Arg Ala Ala Met His Leu Asp Thr Val Phe Ser Phe Cys Asp Arg
 275 280 285

Asp Leu Val Thr Val Phe Pro Glu Val Val Lys Glu Ile Val Pro Phe
290 295 300

Ser Leu Arg Pro Asp Pro Ser Ser Pro Tyr Gly Met Asn Ile Arg Arg
305 310 315 320

Glu Glu Lys Thr Phe Leu Glu Val Val Ala Glu Ser Leu Gly Leu Lys
325 330 335

Lys Leu Arg Val Val Glu Thr Gly Gly Asn Ser Phe Ala Ala Glu Arg
340 345 350

Glu Gln Trp Asp Asp Gly Asn Asn Val Val Cys Leu Glu Pro Gly Val
355 360 365

Val Val Gly Tyr Asp Arg Asn Thr Tyr Thr Asn Thr Leu Leu Arg Lys
370 375 380

Ala Gly Val Glu Val Ile Thr Ile Ser Ala Ser Glu Leu Gly Arg Gly
385 390 395 400

Arg Gly Gly Gly His Cys Met Thr Cys Pro Ile Val Arg Asp Pro Ile
405 410 415

Asp Tyr

(2) INFORMATION FOR SEQ ID NO: 11:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1014 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATGTATCAAT GGAAATACG CAACGACCAT CGTTTGATTG TGAAATCAGA GCCAAATATC	60
GTTGGTTTAT GACGGATTCC TACGTCGCTG CTGCCCGTCT AGGGTCACCT GCACGCCGCA	120
CCCCCGGAC GCGGCGSTAT GCAATGACCC CGCCGGCCTT CTTTGGCGTC GCATACGCGA	180
TCAACCCCTG GATGGACGTC ACCGCGCCAG TCGACGTCCA AGTCGCGCAA GCACAGTGGG	240
AGCACCTCCA CCAGACCTAT CTTCGGCTAG GCCACAGCGT GGATCTGATC GAGCCCATTT	300
CCGGGTTACC GGACATGGTG TACACCGCCA ACGGTGGGTT CATCGCGCAC GACATCGCGG	360

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TGGTCCCGG GTTCGGTTC CCGAACGAG CTGGTGAGTC TAGAGCTAT GCCAGCTGGA 420
TGTCTCGGT CGATATCGC CCGTGACCA CCCGCCAGT CAACGAGGA CAGGGCGACC 480
TGCTGATGT TGGGAAAGG GTGTTGGCG GCTACGGCTT TCACACAGAC CAGCGCGAC 540
ACGCCGAAAT CGCCGCGTG CTGGTCTGC CCGTGCTCTC CCTCGAGTTG GTCGACCCAC 600
GGTTCTATCA CCGGACACC GCGTGCGCG TECTCGACGA CCACACGATC GCTACTACC 660
CGCCGCGCTT CAGTACGGA GCGCAGAAC AGTTGTGGC GCTGTTCCTC GACGCGATTG 720
TGGTCGCGAG TGGGACGCG TTCGTGTCG GACTCAACGC CGTCTCTGAC GGTCTGAACG 780
TAGTGCTTCC GGTGCGGCC ATGGGTTTTG CCGCGCACTT ACGCGCAGCC GGCTTCGAGC 840
CGGTCGGTGT CGATCTGTC GAGCTGCTCA AGGCGCGCGG TTCCGTCAAG TGCTGCACGC 900
TGGAGATACA CCCATGACAA ATCTCGCGGA TGCCACTCAG GCCACTATGG CACTGGTCTGA 960
AAGGCATGCA GCGACAATT ATTCGCCGCT GCCTGTGGTG GCGGCCAGCG CTGA 1014

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(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

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Asn Val Ser Met Glu Asn Thr Gln Arg Pro Ser Phe Asp Cys Glu Ile
1           5           10          15
Arg Ala Lys Tyr Arg Trp Phe Met Thr Asp Ser Tyr Val Ala Ala Ala
20          25          30
Arg Leu Gly Ser Pro Ala Arg Arg Thr Pro Arg Thr Arg Arg Tyr Ala
35          40          45
Met Thr Pro Pro Ala Phe Phe Ala Val Ala Tyr Ala Ile Asn Pro Trp
50          55          60
Met Asp Val Thr Ala Pro Val Asp Val Gln Val Ala Gln Ala Gln Trp
65          70          75          80
Glu His Leu His Gln Thr Tyr Leu Arg Leu Gly His Ser Val Asp Leu
85          90          95

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Ile Glu Pro Ile Ser Gly Leu Pro Asp Met Val Tyr Thr Ala Asn Gly
100 105 110

Gly Phe Ile Ala His Asp Ile Ala Val Val Ala Arg Phe Arg Phe Pro
115 120 125

Glu Arg Ala Gly Glu Ser Arg Ala Tyr Ala Ser Trp Met Ser Ser Val
130 135 140

Gly Tyr Arg Pro Val Thr Thr Arg His Val Asn Glu Gly Gln Gly Asp
145 150 155 160

Leu Leu Met Val Gly Glu Arg Val Leu Ala Gly Tyr Gly Phe Arg Thr
165 170 175

Asp Gln Arg Ala His Ala Glu Ile Ala Ala Val Leu Gly Leu Pro Val
180 185 190

Val Ser Leu Glu Leu Val Asp Pro Arg Phe Tyr His Leu Asp Thr Ala
195 200 205

Leu Ala Val Leu Asp Asp His Thr Ile Ala Tyr Tyr Pro Pro Ala Phe
210 215 220

Ser Thr Ala Ala Gln Glu Gln Leu Ser Ala Leu Phe Pro Asp Ala Ile
225 230 235 240

Val Val Gly Ser Ala Asp Ala Phe Val Phe Gly Leu Asn Ala Val Ser
245 250 255

Asp Gly Leu Asn Val Val Leu Pro Val Ala Ala Met Gly Phe Ala Ala
260 265 270

Gln Leu Arg Ala Ala Gly Phe Glu Pro Val Gly Val Asp Leu Ser Glu
275 280 285

Leu Leu Lys Gly Gly Gly Ser Val Lys Cys Cys Thr Leu Glu Ile His
290 295 300

Pro
305